PLANT BREEDING

Forage peanut genetic variability: Multi-trait selection for forage production and ornamental purposes

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ABSTRACT. The selection of superior genotypes considering several traits simultaneously allows the release of more adapted, productive, and nutritive cultivars. To select forage peanut genotypes for use as animal feed and for ornamental purposes, 67 genotypes were evaluated. Twelve agronomic and nutritive value traits were evaluated in three temporally separated trials: a randomized complete block design. The mixed model method (Restricted Maximum Likelihood/Best Linear Unbiased Prediction (REML/BLUP)) was employed for estimating genetic parameters and predicting genotypic values, which were used in the selection indexes. The selection criteria considered vegetative and seed propagation traits corresponding to the use of forage peanut as animal feed and for ornamental purposes. Seed productivity was also evaluated and correlated with other traits. Genetic variability with high heritability in seed production was observed. Plant vigor, ground cover, and dry matter yield were negatively correlated with seed production. Among the genotypes evaluated, there is a possibility of selecting 14 and 16 genotypes corresponding to seed propagation for animal feed and ornamental purposes, respectively. For vegetative propagation, there are 16 and 14 promising genotypes for animal feed and ornamental purposes, respectively. Vegetatively propagated genotypes generally performed better in terms of agronomic traits related to feed production.

Keywords: *Arachis pintoi* and *A. repens*; breeding program; genetic variability; selection index.

Introduction

Improvements in management, animal breeding, and nutritional practices have led to an increase in productivity in the livestock industry. In addition, genetic breeding of feed species has improved production systems (Valle, Jank, & Resende, 2009). Besides the incorporation of these technologies, the mixed pastures with legumes, particularly forage peanut, have provided important benefits in livestock production (Assis, Valentim, & Andrade, 2013; Pereira et al., 2015; Pereira et al., 2019; Olivo et al., 2019).

Forage peanut (particularly *Arachis pintoi* Krapov. & W. C. Greg. and *Arachis repens* Handro) is a legume with large genetic variability in agronomic traits (Carvalho, Pizarro Juncal, & Valls, 2009; Menezes et al., 2012; Fernandes et al., 2017). The species also has high nutritional stability. However, some variabilities can only be exploited in more advanced stages of breeding programs (Resende, Valle, & Jank, 2008; Ferreira et al., 2012; Simeão, Assis, Montagner, & Ferreira, 2017).

The recently developed forage peanut breeding program seeks the constant development of highly productive cultivars that are adapted and resistant to biotic and abiotic stresses (Assis et al., 2013; Simeão et al., 2017). During the evaluation stages, several traits are evaluated simultaneously to develop superior cultivars in a process called multi-trait selection.

Multi-trait selection allows the definition and application of indices that use all relevant information to rank genotypes (Resende, 2002; Simeão et al., 2017). The multi-trait selection for forage peanut showed promising results (Assis, Valentim, Carneiro Júnior, Azevedo, & Ferreira, 2008; Fernandes et al., 2017; Simeão et al., 2017). However, seed production was ignored. The use of forage peanut for ornamental purposes has also not been studied in detail (Veiga, Valls, Tombolato, Barbosa, & Pires, 2003), despite gaining interest. This use also requires, in addition to the desired traits for feed production, properties such as good visual appearance and ground cover, and an elevated number of flowers, which are highly valued in landscaping.

For both uses, the production and continuous availability of seeds can reduce implantation costs, particularly in large areas. Species implantation is currently conducted vegetatively through stolons and involves high costs because of the low supply of imported seeds, restricting its adoption (Assis et al., 2013).

Therefore, this study selected forage peanut genotypes based on genotypic values for use as animal feed and ornamental purposes, aiming at vegetative and seed propagation for both uses.

Material and methods

Sixty-six forage peanut genotypes from the Active Germplasm Bank located at Embrapa Acre in Rio Branco, Acre State, Brazil were evaluated in three different trials, beginning in December 2005 and ending in April 2013. Each trial was conducted at the same site but was time-separated, and the evaluations consisted of measuring the agronomic traits of the aerial biomass. The local climate is hot and humid equatorial type, characterized by high temperatures, with average temperatures of maximum 31 °C and minimum 21 °C; relative humidity about 80%; and high rainfall, about 1,900 mm per year (Acre, 2010). The rainy season extends from October to April, and the water deficit occurs from June to September.

The experimental area fertilization was performed based on pasture fertilization and liming, according to soil analysis for each trial. The Trial I was installed in Dystrophic Ultisol and the Trial II and III were installed in Dystrophic Oxisol (Embrapa, 2018).

Harvests were made after the establishment period, which for Trial I was 10 months after planting and for Trials II and III was 4 months. The nutritive (bromatological) analyses were performed with 70 days mean of regrowth in dry and rainy seasons.

The three trials were vegetatively implanted, with two stolons per pit and 0.5 m between pits and between rows. To standardize, each stolon was about 25 cm long with five internodes, which three were covered with soil. In Trial II, cv. BRS Mandobi was also implanted by seed with 0.5 m between pits and rows with two seeds per pit. All the trials had as control the cultivars BRS Mandobi and Belmonte vegetatively propagated and were conducted in a randomized complete block design, with four replications for Trial I and III and five replications for Trial II. The trials had 1 m^2 plot of usable area.

The following agronomic traits were evaluated: occurrence of pests and diseases, plant vigor, flowering, ground cover (GC) (obtained visually using a grading scale, according to increasing intensity observed for each trait, adapted from Menezes et al. (2012)), total and leave dry matter yield (TDMY and LDMY) (estimated in kg ha^{-1} after aerial biomass harvest), and seed production (in kg ha^{-1} at the end of each experimental trial). Nutritive value traits used in the study were neutral detergent fiber (NDF) and acid detergent fiber (ADF) (in kg ha^{-1} of dry matter by Georing & Van Soest, 1970) and crude protein content (CP) (in kg ha^{-1} of dry matter by Silva & Queiroz, 2001). The data were analyzed using mixed models, using restricted maximum likelihood (REML) (Patterson & Thompson, 1971) to estimate the variance components and the best linear unbiased prediction (BLUP) (Henderson, 1975) to predict genotypic values. Details on the parameter estimates and their interpretations and classifications are described in Part 1 of this study.

The adopted models were based on those proposed by Resende (2002) for analyzing unrelated perennial plants with one observation per plot. For each trial, a joint analysis was conducted for all harvests and evaluations, considering the repeatability model: $y = Xu + Zg + Wp + Tm + e$; where y is the data vector, u is the vector of the effect of evaluation-repetition combinations (considered fixed) plus the general mean, g is the vector of genotypic effects (considered random), p is the vector of permanent environment effect (plots, considered random), m is the vector of the genotype x evaluations interaction effects, and e is the vector of errors or residuals (random). Capital letters represent the incidence matrices for these effects. For the seed production and nutritive value traits of Trial I, with only one evaluation, the one-site evaluation model was used: $y = Xr + Zg + e$; where y is the data vector, r is the vector of repetition effects (considered fixed) plus the general mean, g is the vector of genotypic effects (considered random), and e is the vector of errors or residuals (random). Capital letters represent the incidence matrices for these effects.

Because of the effect of serial correlation, intrinsic to repeated measurement data, several residual structures for the repeatability model were tested and selected by the likelihood ratio test (LRT) and the Akaike (AIC) and Bayesian Information (BIC) criteria, observed for each matrix in the models where convergence can be found (Littlel, Pendergast, & Natarajan, 2000). The variance components matrix, unstructured matrix (first-order) and analytical factor matrix (first-order) were selected.

The variance components obtained by the REML method for each analysis were used to estimate the respective genetic parameters (heritabilities, repeatabilities, coefficients of determination, coefficients of variation, and correlations), according to Holland, Nyquist, and Cervantes-Martinez (2003) and Resende (2002). The genotypic, permanent plot and genotype x evaluations interaction variabilities, according to each model, were tested by the deviance analysis, also based on the LRT test, according to Resende (2007). This test subtracts the functions -2Log$_e$L, where L is the likelihood equation of the complete model and of the model without the tested effect, and compares this difference to the tabulated χ^2 value. If the value is significant, the tested effect has variability. The same procedure is applied for selecting the residual structure matrices. The results of the joint analysis of all evaluations over the year served as the basis for ranking the genotypic values for each trait, using the BLUP method. Pearson's correlation of the genotypic values was estimated using the t-test at 5 and 1% probabilities and the selection indexes.

The selection objectives for ornamental purposes were increased flowering, plant vigor, and ground cover, and for use as animal feed were to increase TDMY, plant vigor, and ground cover. For both ornamental purposes and feed production, genotypes with high and low seed production were sought to meet the demands of seed sowing and seedling planting (vegetative propagation), respectively.

Table 1 summarizes the selection criteria for each objective. Some characteristics analyzed were discarded because of the low variability or the significant correlations of moderate to high magnitudes with the traits used in this step, according to the results observed .

Table 1. Selection criteria for different purposes used to select forage peanut genotypes in the three trials. Rio Branco, Acre State, Brazil.

Purpose	Ornamental		Forage	
Propagation	Seed	Vegetative	Seed	Vegetative
	Flower	Flower	TDMY	TDMY
Criteria	Vigor	Vigor	Vigor	Vigor
	GC	GC	GC	GC
	SP	-	SP	-

Flower: flowering on a scale from 0 to 10; vigor: visual scale from 0 to 9; GC: % ground cover; SP: seed production, kg ha^{-1}; TDMY: total dry matter yield for each harvest, kg ha^{-1}.

The selection index was based on the sum of ranks (Mulamba & Mock, 1978) and the weight-free index (Elston, 1963). Both indices were modified using genotypic values instead of phenotypic means. In the index based on the sum of ranks, the sum was replaced by the average of ranks, as used in a previous study (Resende, Freitas, Lanza, Resende, & Azevedo, 2014). Furthermore, seed production was assigned twice the weight of the other traits. When used as forage for vegetative propagation, the weight of TDMY was doubled. In the index of ranks, only genotypes with genotypic values above the mean for the main criteria (seed production, flowering, and TDMY) were considered according to the ranking order. This procedure resulted in different proportions of the selected genotypes in each trial and objective. For the weight-free index, the general mean of each trait in their respective trials was employed as the minimum value, except for seed production in Trial I. In this trial, because of the reduced value of the general average, seed production of cv. BRS Mandobi was used as the minimum value.

The gains were calculated based on the mean genotypic values, following Resende (2002). The analyses were conducted in the SAS® program using the PROC MIXED commands for mixed models and PROC CORR for correlations (SAS, 2010), with the aid of an electronic calculation spreadsheet for the indexes.

Results and discussion

Variability and genotypic values

There was genotypic variability in the joint analysis of all evaluations over the years for most traits in the three trials, except for fiber in acid detergent (ADF) and neutral detergent (NDF) for Trial I and NDF for Trial II (Table 2).

According to the heritability classification criterion proposed by Resende (2002), only CP from Trial I showed high magnitude heritability. This highlights the importance of evaluating genotypes by genotypic value, as pointed by Assis et al. (2008), and not just by phenotypic averages.

The inheritance estimated in the broad sense considers the additive and dominance genetic variances, which are especially important in the breeding of vegetative propagation plants, as in this stage of the

improvement program of forage peanut, since the genotype is fully inherited. In addition, the magnitude of heritability determines the difficulty level in improving the trait, indicating the most efficient selection strategy (Resende, 2002). In this case, the selection based on the traits focused on forage production and quality, such as vigor, ground cover (GC), height, total (TDMY) and leaves dry matter yield (LDMY) and crude protein (CP), in the trial I and II tends to be more efficient due to the variability among genotypes and greater individual heritabilities observed in each trial.

Table 2. Parameters of the traits, and seed production, in the joint analysis of seasons for the three trials of forage peanut.

Traits[1]	Trial I	Trial II	Trial III
	h^2_g		
Pest	0.04±0.02**	0.11±0.04**	0.10±0.02**
Disease	0.06±0.03**	0.14±0.04**	0.10±0.02**
Vigor	0.40±0.07**	0.21±0.05**	0.18±0.03**
Flower	0.33±0.06**	0.28±0.06**	0.36±0.04**
GC	0.43±0.07**	0.18±0.04**	0.10±0.02**
Height	0.33±0.06**	0.38±0.06**	0.41±0.04**
CP[1]	0.55±0.23*	0.34±0.10**	0.08±0.03**
ADF[1]	0.19±0.13	0.24±0.08**	0.06±0.02**
NDF[1]	0.17±0.13	0.06±0.04	0.11±0.03**
TDMY	0.30±0.06**	0.40±0.07**	0.43±0.05**
LDMY	0.30±0.06**	0.40±0.07**	0.25±0.05**
Parameters[3]	Seed Production[2]		
h^2_g	0.54±0.23**	0.77±0.27**	0.54±0.23**
h^2_m	0.83	0.93	0.82
Ac	0.91	0.96	0.91
CV_g	133.14	105.27	117.12
CV_e	121.83	57.31	108.24
Mean (kg ha^{-1})	47.88	676.36	258.46

[1] Flower: flowering; GC: ground cover %; CP: crude protein content; ADF and NDF: acid and neutral detergent fiber content, respectively; TDMY and LDMY: total and leave dry matter yield per harvest. [2] Only one evaluation. * and ** significant at 5 e 1% by deviance analysis based on LRT test, respectively. [3] Individual heritabilities in broad sense (h^2_g), mean heritabilities of plot (h^{2m}), accuracy of selection (Ac), genetic (CV_g) and residual (CV_e) coefficients of variation to seed production.

Genotypic variability was observed in seed production in the three forage peanut trials (Table 2). Individual heritabilities in the broad sense (h^2_g) were high (> 50%), suggesting greater genetic control of the trait (Resende, 2002), as well as mean heritability of the plot (h^2_m), with magnitudes above 80%.

The environmental (residual) coefficients of variation (CV_e) were very high, reflecting the elevated environmental influence of underground seed harvesting. However, the genetic coefficients of variation (CV_g) were also high, resulting in CV_g/CV_e ratios above unity in all three trials. This, associated with selection accuracies above 90%, indicated a high possibility of gains from the selection of these traits (Vencovsky, 1987).

The genotypic means of seed production varied among the trials, with the highest production in Trial II (above 670 kg ha^{-1}). Carvalho et al. (2009) observed phenotypic values of up to 3,700 kg ha^{-1} in wetter Cerrado soil. However, these authors observed an 87% reduction in the production of the same genotype in poorly fertile soil, with a decrease in the general phenotypic mean of 1,140 kg ha^{-1} of seeds in an entisol to 396 kg ha^{-1} in dystrophic oxisol. Thus, they concluded that productivity is highly dependent on environmental conditions. It is also important to highlight that the experimental plots received successive harvests, which should have reduced seed production. Therefore, the values used in this study are useful for comparing genotypes, but should not be used for the potential seed production of accessions and cultivars.

According to the results presented in Table 2, the nutritive traits and occurrence of pests and diseases, mostly showed minor variability with other agronomic traits, with reduced possibilities of selection gains. Despite the very low coefficients of variation (< 10%), nutritive value traits may demonstrate some variability, particularly between seasons (Menezes et al., 2012; Fernandes et al., 2017). However, a large variability was observed in other traits, as also seen in other studies on this species (Assis et al., 2008; Carvalho et al., 2009; Ferreira et al., 2012; Simeão et al., 2017), which indicates a broad genetic base and corroborates the evaluated accession variation.

The coefficients of genotypic correlation were significant, positive and varied from moderate (0.34 to 0.66) to high magnitude (> 0.67), according to the classification proposed by Resende (2015), among the traits aimed at forage production (vigor, GC, height, TDMY, and LDMY) (Table 3). The correlations were of smaller magnitude only between height and GC and between dry matter yields and GC and vigor in Trial III.

In general, the correlations between variables related to forage production (vigor, height, TDMY, LDMY and GC) were consistent throughout the trials, showing that this set of variables retains well-established and highly responsive relationships to aerial biomass production in forage peanut. The lack of correlation between some traits in some trials may have its origin in punctual correlations throughout the year, in specific dry and rainy seasons, for example.

Table 3. Genotypic correlations between agronomic and nutritive value traits of forage peanut in the Trial I, II and III, in the joint analysis of seasons.

Traits	Pest	Disease	Vigor	Flower	GC	Height	CP	ADF	NDF	TDMY
					Trial I[1]					
Pest	-	-	-	-	-	-	-	-	-	-
Disease	-0.01	-	-	-	-	-	-	-	-	-
Vigor	-0.04	-0.11	-	-	-	-	-	-	-	-
Flower	0.17	0.27	-0.37	-	-	-	-	-	-	-
GC	-0.11	0.04	0.91**	-0.31	-	-	-	-	-	-
Height	0.57**	-0.13	0.56**	0.02	0.35	-	-	-	-	-
CP	-0.25	-0.30	0.47*	-0.28	0.45*	-0.03	-	-	-	-
ADF	0.36	0.04	-0.13	-0.07	-0.29	0.21	-0.25	-	-	-
NDF	0.27	-0.11	-0.09	-0.43	-0.05	-0.03	-0.11	0.51*	-	-
TDMY	-0.08	-0.17	0.97**	-0.44*	0.89**	0.50*	0.39	-0.13	0.51*	-
LDMY	-0.09	-0.22	0.96**	-0.45*	0.87**	0.48*	0.47*	-0.17	-0.13	0.98**
Seed	0.29	0.11	-0.42	0.20	-0.44*	-0.02	-0.47*	0.14	0.02	-0.47*
					Trial II[2]					
Pest	-	-	-	-	-	-	-	-	-	-
Disease	0.52*	-	-	-	-	-	-	-	-	-
Vigor	-0.63**	-0.90**	-	-	-	-	-	-	-	-
Flower	0.26	0.58*	-0.49*	-	-	-	-	-	-	-
GC	-0.45	-0.84**	0.87**	-0.46	-	-	-	-	-	-
Height	0.62**	-0.07	0.06	-0.06	0.28	-	-	-	-	-
CP	-0.12	-0.38	0.35	0.01	0.20	-0.13	-	-	-	-
ADF	0.41	0.07	0.04	-0.21	0.06	0.48	0.32	-	-	-
NDF	-0.07	-0.60**	0.61**	-0.55*	0.52*	0.28	0.53*	0.59*	-	-
TDMY	-0.21	-0.65**	0.78**	-0.43	0.83**	0.48*	0.08	0.26	0.46	-
LDMY	-0.09	-0.66**	0.74**	-0.48*	0.78**	0.57*	0.14	0.31	0.53*	0.97**
Seed	0.72**	0.41	-0.57**	0.18	-0.41*	0.46**	-0.29	-0.11	-0.38*	0.02
					Trial III[3]					
Pest	-	-	-	-	-	-	-	-	-	-
Disease	0.38*	-	-	-	-	-	-	-	-	-
Vigor	-0.68**	-0.83**	-	-	-	-	-	-	-	-
Flower	0.20	0.07	-0.19	-	-	-	-	-	-	-
GC	-0.24	-0.56**	0.56**	-0.20	-	-	-	-	-	-
Height	0.52**	0.13	-0.29	0.28	-0.32	-	-	-	-	-
CP	-0.20	-0.36*	0.39*	-0.14	0.29	-0.22	-	-	-	-
ADF	0.21	-0.11	-0.05	0.33	-0.19	-0.09	0.02	-	-	-
NDF	-0.31	-0.20	0.28	-0.35*	0.07	-0.60**	0.47**	0.39*	-	-
TDMY	0.32	-0.34*	0.16	0.28	0.31	0.66**	-0.02	0.10	-0.43*	-
LDMY	0.42*	-0.18	0.04	0.23	0.23	0.76**	-0.06	0.00	-0.45**	0.95**
Seed	0.45**	0.39*	-0.57**	0.18	-0.41*	0.46**	-0.29	-0.11	-0.38*	0.02

[1]Trial I: performed between 2006 and 2008; [2]Trial II: performed between the years of 2009 and 2011; [3]Trial III: performed between the years of 2011 and 2013. * and ** significant by Student t test at 5% e 1%, respectively. (-) Missing values or data. Flower: flowering; GC: ground cover, %; CP: crude protein content of aerial biomass; ADF and NDF: acid and neutral detergent fiber content; TDMY: total dry matter yield per harvest; LDMY: leaf dry matter yield per harvest.

Genotypic correlations between agronomic traits and seed production) ranged from low (< 0.33) to moderate (0.33 to 0.66) magnitudes. These magnitudes possibly indicate that a few genes related to seed production directly influence other traits (Resende et al., 2008). In addition, there was a large variation in magnitude and significance among trials, which demonstrates the variable character of the traits associated with the specific environmental conditions detected in each evaluation environment. This variation supports the use of genotypic correlations in breeding programs, which relate the heritable components of each trait to the detriment of widely variable phenotypic correlations (Assis et al., 2008).

Although not always significant, vigor and GC traits showed a moderately negative correlation with seed production, which is unfavorable in the breeding process for use as forage with seed propagation. The correlations of low to moderate magnitudes of TDMY with seed production, despite being significant only in

Trail I, were also negative, corroborating this result. Such negative correlations reinforce the importance of identifying the relationships among the traits of interest, as a change in one via selection promotes a change in the others by correlated responses. This is relevant for determining the traits to be employed in simultaneous selection (Resende, 2002).

The occurrence of pests was significantly positively correlated with seed production in trials II and III, with a higher magnitude in Trial II. There was a medium-magnitude correlation between seed production and disease occurrence, which was significant only in Test III. These results reflect the negative correlation between seed production and TDMY, as this trait is negatively correlated with the occurrence of diseases (Part 1). This contributed to the negative correlation between seed production and vigor (positively correlated with TDMY), as plants can have less vigor due to pests and diseases, which reduce leaf area and, consequently, its photosynthetic process (Viana et al., 2004).

This trend can complicate the selection process aimed at increasing vigor, dry matter production, and seed production. Plants under stress tend to allocate their reserves toward seed production without being able to return the photoassimilates to vegetative development, which negatively affects biomass production (Martiniello, 1998). However, genotypes with positive attributes should be selected in breeding programs. The cultivar BRS Mandobi is a good example (Assis et al., 2013).

The nutritive traits presented significantly negative and medium magnitude correlations only for CP in Trial I and NDF in Trial III, which may be associated with seasonal factors as the other traits were not significantly correlated and of low magnitude with the production of seeds. However, plant height was positively and moderately correlated with seed production in trials II and III. For peanut (*Arachis hypogaea*), plant height is considered a genetic attribute that is highly influenced by environmental factors and may show changes in the correlation with seed production according to environmental conditions, such as soil moisture (Dapaah, Mohammed, & Awuah, 2014; Arruda, Moda-Cirino, Buratto, & Ferreira, 2015).

There was no correlation between seed production and flowering in trials I and III, as previously observed for this species (Argel, 1994; Carvalho et al., 2009). However, seed production in Trial II showed a positive and medium-magnitude correlation with flowering. This correlation indicates that other factors may influence this relationship, such as the genetic composition of the population under evaluation, which was randomly sampled from the germplasm bank.

In the three trials, some genotypes performed better than the commercial controls for most of the traits of interest, indicating the possibility of selection, particularly for *A. pintoi* genotypes (Tables 4 and 5).

Table 4. Genotypic values for agronomic and nutritive traits of forage peanut in Trial I, conducted between 2006 and 2008, and in Trial II, conducted between 2009 and 2011.

	BRA/cultivar	Vigor	Flower	GC	TDMY	Seed
Trial I	014931	5.37	2.88	53.63	1,535.91	228.74
	014991	5.58	2.93	53.47	1,841.81	19.51
	015083	6.62	1.78	89.05	2,546.04	8.60
	030333	6.42	3.48	81.72	1,954.32	113.16
	032352[1]	6.80	2.38	91.10	2,315.84	8.58
	032379[1]	7.14	2.72	94.44	2,709.42	9.61
	032409	6.65	2.78	90.62	2,469.76	13.95
	033260[1]	6.20	0.89	83.73	2,141.98	8.29
	034142	5.15	2.02	57.64	1,717.96	138.24
	034436[1]	5.54	1.78	62.14	1,565.24	8.29
	035033[3]	6.50	3.85	88.50	2,220.62	116.36
	035041[3]	5.76	3.45	62.62	1,497.61	90.13
	035068[2]	6.58	2.91	92.21	2,689.81	27.37
	035114	6.37	3.65	79.83	2,140.55	17.53
	039187	7.74	1.54	97.29	3,231.82	15.23
	039799	8.12	1.96	97.08	3,410.85	15.86
	040894	5.15	3.20	43.67	1,412.15	31.11
	52*	7.81	2.20	96.53	2,961.36	36.67
	Alqueire-1	7.29	2.59	90.63	2,801.57	62.33
	Belmonte	7.76	1.09	97.12	3,232.13	10.03
	BRS Mandobi	6.85	2.11	89.07	2,450.30	25.96
	Mean	6.54	2.49	80.58	2,326.05	47.88
Trial II	012122	6.75	2.37	89.92	1,880.42	972.30
	014982	7.63	1.18	96.99	3,038.18	180.59

029190[1]	7.38	1.82	97.06	2,571.79	41.98
029203[1]	7.24	0.63	95.09	2,099.10	49.41
029220[1]	7.04	2.06	91.96	1,902.37	375.72
030325	6.59	2.29	83.91	1,662.06	1,105.02
030384	7.32	2.93	95.99	2,619.49	178.81
030601	6.89	1.80	94.65	2,309.61	1,681.71
035076[2]	6.71	1.82	89.43	1,950.04	347.55
038857[2]	6.52	1.35	88.28	2,255.64	384.31
039772	6.59	2.95	86.80	1,516.57	1,180.80
039985	7.32	1.96	96.87	2,889.83	523.97
040045	7.31	0.93	96.83	2,589.80	72.78
Amarillo	6.69	2.56	92.19	1,984.36	1,464.68
Belmonte	7.41	0.81	97.07	3,135.20	59.31
BRS Mandobi	6.59	1.88	95.54	2,730.58	1,057.59
BRS Mandobi [(s)]	6.98	2.29	94.41	2,444.71	2,439.90
Mean	7.01	1.78	93.31	2,327.36	676.36

*Local identification (without BRA). [(s)]propagation through seeds. [1]genotypes of *Arachis repens*; [2]hybrids of *A. pintoi* × *A. repens*; [3]crossing of *A. pintoi* × *A. pintoi*. Vigor: visual scale of 0 to 9; Flower: flowering on a scale of 0 to 10; GC: % of ground cover; TDMY: total dry matter yield per harvest, kg ha^{-1}; Seed: seed production, kg ha^{-1}.

Table 5.1 Genotypic values for agronomic and nutritive traits of forage peanut in Trial III, conducted between 2011 and 2013.

BRA/cultivar	Vigor	Flower	GC	TDMY	Seed
012114[1]	7.79	0.31	95.79	1,366.96	215.52
014788[1]	7.76	2.06	90.98	1,687.35	48.38
015121	6.85	1.84	93.17	1,607.35	907.28
016357	6.85	1.37	92.04	1,698.06	744.05
016683	7.01	1.60	93.50	1,470.15	529.04
022683	7.69	2.94	93.92	1,729.76	67.26
030082[1]	7.56	0.59	96.06	1,292.56	45.48
030635	7.54	1.58	95.61	1,792.08	630.76
030872	7.09	1.30	93.97	1,776.93	359.46
030899	7.19	2.59	89.66	1,323.90	129.17
030929	7.50	1.73	96.19	1,973.75	686.97
031275	7.37	1.11	94.97	2,015.14	277.02
031461	6.85	1.37	94.61	1,711.43	720.95
031526	7.21	0.38	94.67	1,914.22	45.48
031909	7.94	0.18	95.80	1,598.07	45.48
031984	7.32	2.06	95.29	1,975.57	176.30
032280[1]	7.34	0.27	95.74	1,838.20	45.48
032280[1]	6.82	0.31	93.03	1,451.40	45.48
032361[1]	7.38	1.17	94.83	1,209.47	45.48
032387[1]	7.80	1.30	96.18	1,874.89	45.48
032409	7.68	1.32	92.71	1,436.73	165.69
032433	6.93	1.33	93.75	1,742.88	359.41
032492[1]	7.51	0.12	94.46	1,515.38	45.48
034355	7.43	0.76	92.52	2,040.28	331.74
034363[1]	7.63	0.25	95.68	1,309.49	45.48
035122	7.15	2.40	93.54	1,976.49	56.95
036544	6.47	0.70	82.30	1,344.67	971.28
037443[1]	7.16	0.59	93.73	1,359.84	46.92
039195	7.14	2.42	93.33	1,998.73	62.62
040088[1]	7.84	0.14	95.72	1,545.76	226.14
040185[1]	7.77	0.21	95.09	1,367.50	45.48
040193	7.61	1.32	95.86	2,068.13	328.21
040223	7.90	1.45	95.79	2,352.24	143.07
Belmonte	7.84	0.44	96.62	2,204.89	45.48
BRS Mandobi	6.83	1.35	95.38	1,755.39	361.65
Mean	7.36	1.17	94.07	1,695.02	258.46

[1]genotypes of *Arachis repens*. Vigor: visual scale of 0 to 9; Flower: flowering on a scale of 0 to 10; GC: % of ground cover; TDMY: total dry matter yield per harvest, kg ha^{-1}; Seed: seed production, kg ha^{-1}.

In general, *A. repens* genotypes showed higher vigor values but with lower seed production and lower TDMY. Inferior TDMY performance has been reported for *A. repens*, with accumulated phenotypic values of up to 8,800 kg ha^{-1} per annum, in contrast to 11,100 kg ha^{-1} of TDMY achieved by *A. pintoi* (Assis et al., 2008; Fernandes et al., 2017).

Belmonte cultivars presented values above the mean for traits related to forage use in all trials, with genotypic values above 3,100 kg ha^{-1} of TDMY per harvest in trials I and II. This cultivar has demonstrated better performance since the establishment phase, with TDMY being superior to the other genotypes, even in periods of lower water availability (Assis et al., 2008). In addition, genotypic values of accumulated TDMY above 8,000 kg ha^{-1} were obtained in the Cerrado region, with GC above 80% over the year for the region (Fernandes et al., 2017; Simeão et al., 2017). However, the cultivar Belmonte rarely produces seeds.

BRS Mandobi, a vegetatively propagated cultivar, showed lower values of vigor, GC, and TDMY than Belmonte, but with superior flowering and high seed production, particularly in trials II and III. Sexually propagated BRS Mandobi produced 60% more seeds than BRS Mandobi propagated by stolons in Trial II, exceeding the genotypic value of 2,400 kg ha^{-1} of seeds, but with a reduction of approximately 10% in TDMY (2,440 kg ha^{-1}). Phenotypic values of up to 3,000 kg ha^{-1} of seeds were reported for this cultivar between 18 to 21 months after planting (Valentim, Assis, & Sá, 2009).

Hybrids are important in breeding programs as they exploit heterosis in the F1 generation, and because they allow an increase in genetic variability (Assis & Valentim, 2013), they show inferior performance for most agronomic traits. *A. repens* genotypes and hybrids are classified as having low to intermediate performance, mainly for GC (Assis et al., 2008). As the hybrids analyzed were obtained by crossing the parental divergent to morphological characteristics, with flower color as one of the most important criteria for selection (Oliveira & Valls, 2002), forage production traits were not considered. For specific conditions, such as more severe periods of drought and cold, tolerant parents aimed at superior agronomic productivity should be selected in each environment of interest, which tends to improve the productive performance of the next hybrid.

Selection for ornamental purposes

In general, the two selection indices used were in agreement with the identification of genotypes for ornamental purposes (Table 6). The weight-free index (Elston, 1963) identified fewer genotypes than the index based on the sum of ranks (Mulamba & Mock, 1978) because of its more rigorous selection process. In this case, the genotype selection was nullified if only one trait was below the selection criteria.

Table 6. Forage peanut genotypes identified for ornamental purposes, aiming at seed and vegetative propagation, according to two selection indexes.

Trial I		Trial II		Trial III		
BRA/Cultivar		BRA/Cultivar		BRA/Cultivar		
Ranks[1]	Free[2]	Ranks	Free	Ranks		Free
Propagation by seeds						
		Mandobi(s)				
035033		Amarilo		030929	Mandobi	030929-030635
030333	030333	030601	Mandobi(s)	030635	016683	031461
035068	035068	039772	Mandobi	040193	016357	040193
Mandobi		Mandobi	030601	015121	030872	Mandobi
		012122		031461	032433	
Vegetative propagation						
				040223		030929
032379	035033	029190	030384	030929	014788	031984
035068	032379	039985	039985	032387	035122	030635
030333	035068	030384	Mandobi(s)	040193	039195	040223
032409	032409	Mandobi	029190	030635	032409	032387
035033	030333	Mandobi 029220	Mandobi	031984	030872	040193
		030601	30601	022683	016683	031462
		012122		032361	030899	032361

[1]Index based on the sum of ranks (Mulamba & Mock, 1978); [2]Weight-free index (Elston, 1963). (s)propagated by seeds.

However, the rank index only orders the genotypic values according to their magnitudes. This allows for selection according to the pre-established intensity (or the desired gains), as there is no previous elimination of genotypes. In this case, the two indices complemented each other as the free index (more restrictive) does not allow the inclusion of genotypes below the criterion value for only one trait of interest, even if these genotypes reveal a high potential for other traits.

There were losses in TDMY when considering propagation by seeds in Trial I (by the free index) and Trial II (by the rank index). GC remained unchanged in trials II and III, with values above 90% (Table 7) and gains of up to 11% in Trial I, showing a wider variation for this trait.

Table 7. Means of the selected genotypes, population, and gains (%), obtained by the selection of forage peanut genotypes for ornamental purposes for seed and vegetative propagation, according to two selection indexes for the three trials.

Index Propagation			Vigor	Flower	GC	TDMY	Seeds
		$\bar{X}S$ [3]	6.54	2.49	80.58	2,326.05	47.88
Trial I	Ranks [1]	Seed	$\bar{X}S$ [4]				
			6.59	3.09	87.87	2,328.76	70.71
		%	0.65	24.15	9.06	0.12	47.68
		Vegetative	$\bar{X}S$				
			6.66	3.15	89.50	2,408.78	56.09
		%	1.75	26.62	11.07	3.56	17.14
	Free [2]	Seed	$\bar{X}S$				
			6.46	3.66	85.11	2,087.47	114.76
		%	-1.27	47.38	5.63	-10.26	139.67
		Vegetative	$\bar{X}S$				
			6.66	3.15	89.50	2,408.78	56.09
		%	1.75	26.62	11.07	3.56	17.14
Trial II		$\bar{X}$	7.01	1.78	93.31	2,327.36	676.36
	Ranks	Seed	$\bar{X}S$				
			6.75	2.31	92.25	2,144.37	1,466.16
		%	-3.77	29.28	-1.13	-7.86	116.77
		Vegetative	$\bar{X}S$				
			7.03	2.14	94.55	2,418.60	909.00
		%	0.32	19.84	1.33	3.92	34.40
	Free	Seed	$\bar{X}S$				
			6.82	1.99	94.87	2,494.97	1,726.40
		%	-2.73	11.44	1.67	7.20	155.25
		Vegetative	$\bar{X}S$				
			7.08	2.11	95.76	2,594.33	987.33
		%	0.98	18.35	2.62	11.47	45.98
Trial III		$\bar{X}$	7.36	1.17	94.07	1,695.02	258.46
	Ranks	Seed	$\bar{X}S$				
			7.10	1.48	94.41	1,759.62	562.77
		%	-3.52	26.78	0.36	3.81	117.74
		Vegetative	$\bar{X}S$				
			7.45	1.82	94.09	1,776.41	231.65
		%	1.18	55.58	0.02	4.80	-10.37
	Free	Seed	$\bar{X}S$				
			7.27	1.47	95.53	1,860.15	545.70
		%	-1.34	25.98	1.55	9.74	111.14
		Vegetative	$\bar{X}S$				
			7.49	1.50	95.55	1,869.69	347.15
		%	1.68	28.26	1.57	10.31	34.32

[1]Index based on the sum of ranks (Mulamba & Mock, 1978); [2]Weight-free index (Elston, 1963); [3]General mean; [4]Mean of selected genotypes. Occurrences of Pest and Disease: visual scale of 0 to 10; Vigor: visual scale of 0 to 9; Flower: flowering on a scale of 0 to 10; GC: % of ground cover; Height: plant height, cm; CP: crude protein content of aerial biomass, kg ha⁻¹; ADF and NDF: acid and neutral detergent fiber content, respectively, kg ha⁻¹; TDMY: total dry matter yield per harvest, kg ha⁻¹; Seed: seed production, kg ha⁻¹.

There were gains in seed production in all cases, except for the rank index for vegetative propagation in Trial III. Likewise, flowering, one of the most relevant traits for ornamentation in this species (Cruz, Suárez, & Ferguson, 1994; Veiga et al., 2003), revealed gains above 20% in all cases, except for the free index for seed propagation in Trial II (11.44%).

Propagation by seeds

The indices reduced the vigor means because of the inverse correlation between vigor and seed production (Table 3), except for Trial I. However, all values were above 6 (Table 7).

Among the genotypes aimed at this type of propagation, only Trial I indicated the presence of hybrids (*A. pintoi* intraspecific BRA 035033 with high seed production and *A. pintoi* × *A. repens* interspecific BRA 035068 with high GC but lower seed production, thus disregarded for this type of propagation). The BRA 030333 genotype, with high flowering, was also indicated, which increased by up to 47% of the flowering means of the genotypes selected according to the free index (Table 7).

Trial II identified highly productive seed genotypes such as cv. Amarillo and BRA 030601. The BRA 039772 and 012122 genotypes, with lower vigor and GC, were also identified in this trial, causing a minor decrease in GC according to the rank index. However, the mean coverage remained above 90% (Table 7).

In Trial III, the two indices identified genotypes BRA 030929, 030635, 040193, and 031461 (Table 6). The rank index also identified genotypes with good flowering (BRA 015121 and 030872). The BRA 016683, 016357, and 032433 genotypes were also identified, all with vigor below the trial population mean, although the values remained above 7.

Vegetative propagation

BRS Mandobi was identified in all three trials for its elevated seed production capacity (Assis et al., 2013), with values above the mean for this trait in trials II and III. However, the production of this cultivar was lower than expected in Trial I, which was possibly the result of harvesting conducted soon after the last evaluation harvest and during the rainy period. In general, this may have affected the fruit accumulation rate and stimulated the recruitment of new individuals, thus reducing the number of harvested seeds. Consequently, the mean seed production in this trial was low (Table 4).

Several genotypes were identified when considering vegetative propagation, which increased the variability for the interest traits, as most of these genotypes were also related to propagation by seeds (Table 7).

Trial I identified the genotypes BRA 032409, *A. repens* BRA 032379, and BRA 035068. Trial II identified *A. repens* (BRA 029190 and 029220) and *A. pintoi* (BRA 039985 and 030384). In Trial III, more genotypes concerning seed propagation were identified (*A. repens* BRA 032387, 032361, and 014788, with high flowering and vigor). In addition, genotypes BRA 040223 and 031984, with high TDMY and GC, and BRA 022683, 035122, and 039195, with high flowering, increased the flowering means by up to 55% (Table 7). However, the BRA 032361 genotype was not considered for selection because of its low TDMY and GC values.

BRS Mandobi was identified only in Trial II because of its high flowering and GC values. In addition, *A. repens* genotypes were included in the three trials as the seed production of this species is lower than that of *A. pintoi* (Ramos, Barcellos, & Fernandes, 2010). However, Veiga et al. (2003) observed that *A. repens* performs better than *A. pintoi* in landscaping use, mainly because of its visual appearance, greater flowering, and elevated ability to survive in unfavorable conditions. For both propagation types, Alqueire-1, which has high flowering, vigor, and GC and is highly productive and adapted to the southern region of the country (Ramos et al., 2010), was not indicated for use in ornamentation because of its multiple genetic origins. According to Ramos et al. (2010), there is high phenotypic variability within the cultivar, arising from a mixture of several accessions. This tends to form visually uneven plots that are not ideal for ornamental use.

Selection for forage use

The indices were also in agreement with respect to most of the genotypes identified for forage production (Table 8). Belmonte was identified in all trials aimed at vegetative propagation, and BRS Mandobi was suitable for seed propagation. A higher selection difficulty was observed considering propagation by seeds in trials I and II because of the inverse correlation of TDMY with seed production in these trials (Table 3). This resulted in a reduced number of genotypes for this form of propagation.

Table 8. Forage peanut genotypes identified for forage production, aimed at seed and vegetative propagation according to two selection indexes.

Trial I		Trial II		Trial III		
BRA/Cultivar		BRA/Cultivar		BRA/Cultivar		
Ranks[1]	Free[2]	Ranks	Free	Ranks	Free	
Propagation by seeds						
52				030929		031461
Alqueire-1	52			040193	Mandobi	030635
035033	Alqueire-1	Mandobi[s]	Mandobi[s]	030635	030872	030929
035068	035068	Mandobi	Mandobi	031275	032433	040193
Mandobi	Mandobi	030601		034355	016357	031275
Vegetative propagation						
039799	039799					
Belmonte	Belmonte	Belmonte	Belmonte			Belmonte
139187	039187	014982	014982	Belmonte	031984	040223
52	52	030384	039985	040223	030635	032387
032379	Alqueire-1	029190	029190	040193	032280	040193
Alqueire-1	032379	Mandobi[s]	040045	032387	034355	030929
035038	Mandobi	Mandobi	030384	030929	031526	030635
032409	035068	039985	Mandobi[s]	031275	039195	031275
Mandobi	032409	040045	Mandobi			
015083	015083					

[1]Index based on the sum of ranks (Mulamba & Mock, 1978); [2] Weight-free index (Elston, 1963). [s]propagated by seeds.

Flowering presented reduced means in Trials I and II by vegetative selection, and the height and TDMY mean traits revealed gains in all cases. Vegetative propagation selection caused a decrease in seed production means in trials I, II, and III according to the rank index.

Propagation by seeds

The cultivars Alqueire-1 and BRS Mandobi were identified (the former in Trial I and the latter in all three trials) for high TDMY and high seed production, particularly if BRS Mandobi was propagated by seeds (Table 8). This resulted in a loss of vigor in trials II and III by the rank index, and expressive gains in GC only in Trial I, reaching approximately 16% (Table 9).

Table 9. Means of the selected genotypes, population, and gains (%), obtained by the selection of forage peanut genotypes for forage production aimed at seed and vegetative propagation, according to two selection indexes for the three trials.

	Index	Propagation		Vigor	Flower	GC	TDMY	Seed
			$\overline{X}$ [3]	6.54	2.49	80.58	2,326.05	47.88
Trial I	Ranks[1]	Seed	$\overline{X}$S [4]	7.01	2.73	91.39	2,624.73	53.74
			%	7.07	9.88	13.42	12.84	12.23
		Vegetative	$\overline{X}$S	7.26	2.17	93.41	2,850.30	22.56
			%	10.89	-12.76	15.92	22.54	-52.88
	Free[2]	Seed	$\overline{X}$S	7.13	2.45	92.11	2,725.76	38.08
			%	8.99	-1.36	14.32	17.18	-20.47
		Vegetative	$\overline{X}$S	7.26	2.17	93.41	2,850.30	22.56
			%	10.89	-12.76	15.92	22.54	-52.88
Trial II			$\overline{X}$	7.01	1.78	93.31	2,327.36	676.36
	Ranks	Seed	$\overline{X}$S	6.82	1.99	94.87	2,494.97	1,726.40
			%	-2.73	11.44	1.67	7.20	155.25
		Vegetative	$\overline{X}$S	7.24	1.73	96.35	2,752.45	569.37
			%	3.30	-3.32	3.26	18.26	-15.82
	Free	Seed	$\overline{X}$S	6.78	2.08	94.98	2,587.65	1,748.75
			%	-3.27	16.82	1.79	11.18	158.55
		Vegetative	$\overline{X}$S	7.24	1.73	96.35	2,752.45	569.37
			%	3.30	-3.32	3.26	18.26	-15.82
Trial III			$\overline{X}$	7.36	1.17	94.07	1,695.02	258.46
	Ranks	Seed	$\overline{X}$S	7.20	1.32	94.49	1,857.41	480.02
			%	-2.24	13.31	0.45	9.58	85.72
		Vegetative	$\overline{X}$S	7.50	1.23	95.23	2,004.01	234.88
			%	1.85	5.75	1.23	18.23	-9.12
	Free	Seed	$\overline{X}$S	7.50	1.43	95.66	1,962.27	480.74
			%	1.91	22.85	1.69	15.77	86.00
		Vegetative	$\overline{X}$S	7.65	1.27	95.89	2,040.16	308.14
			%	3.89	9.16	1.93	20.36	19.22

[1]Index based on the sum of ranks (Mulamba & Mock, 1978); [2]Weight-free index (Elston, 1963); [3]General mean; [4]Mean of selected genotypes. Occurrences of Pest and Disease: visual scale of 0 to 10; Vigor: visual scale of 0 to 9; Flower: flowering on a scale of 0 to 10; GC: % of ground cover; Height: plant height, cm; CP: crude protein content of aerial biomass, kg ha^{-1}; ADF and NDF: acid and neutral detergent fiber content, respectively, kg ha^{-1}; TDMY: total dry matter yield per harvest, kg ha^{-1}; Seed: seed production, kg ha^{-1}

Genotype 52 and hybrids BRA 035033 and 035068 (both hybrids already listed for ornamental purposes) were also identified in Trial I, which suggests the possibility of using these genotypes for dual purposes. However, the identification of BRA 035068 caused a decrease of approximately 20% in mean seed production for genotypes selected by the free index. This hinders species improvement as its low adoption in larger areas is related to the difficulty and costs of planting by stolons (Assis et al., 2013). Therefore, BRA 035068 was disregarded for this type of propagation.

In Trial II, the BRA 030601 genotype was identified. In Trial III, in addition to the previously mentioned genotypes for ornamental use, the BRA 031275 and 034355 genotypes were also identified, all with a TDMY above 2,000 kg ha^{-1}, resulting in gains of up to 15.77% for this trait (Table 9). The indication of genotypes for both ornamental and forage use opens new market perspectives for the release of new cultivars because the dual purpose of future cultivars enables higher adoption rates, meeting specific consumption and production demands.

Vegetative propagation

The selection considering vegetative propagation by stolons showed an elevated number of genotypes, which indicates a greater chance of success. There was also an indication of some genotypes already

mentioned for seed propagation, mainly in Trial III (Table 8), which increased the variability of the groups. This type of propagation increased the gains in vigor and TDMY means, except in Trial III (Table 9).

In Trial I, 10 genotypes were identified, including Belmonte and the BRA 039799 and 039187 genotypes, all with high TDMY and superior performance in the Cerrado region (Fernandes et al.; 2017; Simeão et al., 2017). This inclusion resulted in gains of more than 22% for TDMY and 15.92% for GC among the selected genotypes (Table 9). In Trial II, both indices indicated that the genotypes BRA 014892, 039985, 030384, 040045, and *A. repens* BRA 029190, all with elevated TDMY, in addition to the cultivars Belmonte and BRS Mandobi, increased TDMY means by 18.26%.

In Trial III, the genotypes selected were BRA 04223, 04193, 030929, 030635, 031275, and *A. repens* BRA 032387 were identified, in addition to cv. Belmonte. The rank index identified five more genotypes (BRA 031984, 034355, 031526, 039195, and *A. repens* BRA 032280), all with TDMY above 1,800 kg ha^{-1}, increasing the selected genotype means by up to 18.23%. In this trial, the gains for GC were minor, although the means remained above 95% (Table 9).

The number of *A. repens* genotypes identified was also elevated for vegetative propagation, reinforcing the tendency of inferior seed production of the species related to *A. pintoi*. In addition, *A. repens* genotypes revealed the potential for elevated TDMY, which has already been observed for BRA 032379 in drier regions (Simeão et al., 2017).

Thus, the selection of superior genotypes is facilitated by the use of indices that balance the traits employed in the selection criteria. In this manner, the genotypes that will compound the next selection cycle present the necessary conditions for the continuity of the breeding program: the presence of genetic variability and superior performance.

The subsequent step of the species breeding program may thus include the selection of more adapted ecotypes by regional experiments, such as trials conducted in the Cerrado region (Fernandes et al., 2017; Simeão et al., 2017). Another step includes parental selection for hybridization and generation advancement in the Amazon region (Assis & Valentim, 2013).

The selected genotypes should be directed toward the most promising combinations of selection objectives, which must be based on agronomic and nutritive performance. This will increase the chance of selecting more adapted and productive genotypes, including forage production (converted into animal productivity), ground cover, and ornamental use, as well as for dual purposes.

Conclusion

There is genetic variability among the accessions of the Active Germplasm Bank of Forage Peanut, providing a favorable condition for selection aimed at forage production and ornamental purposes, with both vegetative and seed propagation. Generally, vegetatively propagated genotypes exhibit superior performance for agronomic traits related to forage production (vigor, ground cover, and dry matter production), indicating that selection should consider propagation forms separately. Genotypes with a dual-purpose potential have been identified for the continuity of evaluations in breeding programs for both forage production and ornamental use, considering the two propagation forms.

Acknowledgements

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